We claim:

1. A method for the transgenic expression of nucleic acid sequences in the flower of plants, including the following steps

   I. introduction of a transgenic expression cassette into plant cells, where the transgenic expression cassette comprises at least the following elements

      a) at least one promoter sequence of a gene coding for an ε-cyclase, and

      b) at least one further nucleic acid sequence, and

      c) where appropriate further genetic control elements,

      where at least one of said promoter sequences and one further nucleic acid sequence are functionally linked together, and the further nucleic acid sequence is heterologous in relation to the promoter sequence or the plant cell, and

   II. selection of transgenic cells which comprise said expression cassette stably integrated into the genome, and

   III. regeneration of complete plants from said transgenic cells, where at least one of the further nucleic acid sequences is expressed in the flower.

2. The method as claimed in claim 1, where the promoter sequence of a gene coding for an ε-cyclase is a sequence selected from the group of sequences consisting of

   i) the promoter sequence of the ε-cyclase from Tagetes erecta as shown in SEQ ID NO: 1, the ε-cyclase from Arabidopsis thaliana as shown in SEQ ID NO: 7, the ε-cyclase from Oryza sativa as shown in SEQ ID NO: 8, and

ii) functional equivalents of the promoter sequences as shown in SEQ ID NO: 1, 7 or 8 having substantially the same promoter activity as the promoter of the ε-cyclases as shown in SEQ ID NO: 1, 7 or 8 and

iii) functionally equivalent fragments of the sequences under i) or ii) having substantially the same promoter activity as the promoter of ε-cyclases as shown in SEQ ID NO: 1, 7 or 8.

3. A method for identifying and/or isolating promoters of genes which code for an ε-cyclase, where at least one nucleic acid sequence or a part thereof is employed in the identification and/or isolation, where said nucleic acid sequence codes for an amino acid sequence which comprises at least one sequence as shown in SEQ ID NO: 17, 18, 19, 20, 21 or 22 or a variation of these sequences.

4. The method as claimed in claim 3, where said nucleic acid sequence comprises a sequence as shown in SEQ ID NO: 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43 or 45.

5. The method as claimed in either of claims 3 or 4, where the method is carried out with use of the polymerase chain reaction, and said nucleic acid sequence or a part thereof is employed as primer.

6. A method for producing a transgenic expression cassette with specificity for the flower of plants, including the following steps:

I. isolation of a promoter sequence, where at least one nucleic acid sequence or a part thereof is employed in the isolation, where said nucleic acid sequence codes for an amino acid sequence which comprises at least one sequence as shown in SEQ ID NO: 17, 18, 19, 20, 21 or 22 or a variation of these sequence motifs.

II. functional linkage of said promoter sequence to a further nucleic acid sequence, where said nucleic acid sequence is heterologous in relation to the promoter.

7. The method as claimed in claim 6, where said nucleic acid sequence includes a sequence as shown in SEQ ID NO: 23, 25, 27, 29, 29, 31, 33, 35, 37, 39, 41, 43 or 45.

8. The method as claimed in either of claims 6 or 7, where the method is carried out with use of the polymerase chain reaction, and said nucleic acid sequence or a part thereof is employed as primer.

9. A transgenic expression cassette for the targeted transgenic expression of nucleic acid sequences in the flower of plants, including

a) at least one promoter sequence of a gene coding for an ε-cyclase, and

b) at least one further nucleic acid sequence, and

c) where appropriate further genetic control elements,

where at least one promoter sequence and one further nucleic acid sequence are functionally linked together, and the further nucleic acid sequence is heterologous in relation to the promoter sequence.

10. The transgenic expression cassette as claimed in claim 9, where the promoter sequence of a gene coding for an ε-cyclase is a sequence selected from the group of sequences consisting of

i) the promoter sequence of the ε-cyclase from Tagetes erecta as shown in SEQ ID NO: 1, the ε-cyclase from Arabidopsis thaliana as shown in SEQ ID NO: 7, the ε-cyclase from Oryza sativa as shown in SEQ ID NO: 8, and

ii) functional equivalents of the promoter sequences as shown in SEQ ID NO: 1, 7 or 8 having substantially the same promoter activity as the promoter of the ε-cyclases as shown in SEQ ID NO: 1, 7 or 8 and

iii) functionally equivalent fragments of the sequences under i) or ii) having substantially the same promoter activity as the promoter of ε-cyclases as shown in SEQ ID NO: 1, 7 or 8.

11. The transgenic expression cassette as claimed in claim 9 or 10, where the nucleic acid sequence to be expressed transgenically enables

a) the expression of a protein encoded by said nucleic acid sequence, or

b) the expression of a sense RNA, antisense RNA or double-stranded RNA encoded by said nucleic acid sequence.

12. An isolated nucleic acid sequence comprising

a) the Tagetes erecta ε-cyclase promoter as shown in SEQ ID NO: 1 or

b) a functionally equivalent fragment of a) with substantially the same promoter activity as a).

13. The isolated nucleic acid sequence as claimed in claim 12, including, in the 3' orientation to the Tagetes erecta ε-cyclase promoter as shown in SEQ ID NO: 1 or a functionally equivalent fragment of the aforementioned, a sequence coding for a 5'-untranslated region and/or a transit peptide.

14. The isolated nucleic acid sequence as claimed in claim 12 or 13 including a sequence described by SEQ ID NO: 2 or 3.

15. A double-stranded RNA molecule comprising

a) a sense RNA strand comprising at least one ribonucleotide sequence which is substantially identical to at least part of a nucleic acid sequence coding for the promoter region of an ε-cyclase, and

b) an antisense RNA strand which is substantially complementary to the RNA sense strand under a).

16. The double-stranded RNA molecule as claimed in claim 15, where the promoter region of the ε-cyclase comprises a sequence selected from the sequences as shown in SEQ ID NO: 1, 7 or 8.

17. A ribonucleic acid molecule comprising

a) at least one ribonucleotide sequence which is substantially identical to at least one part of a nucleic acid sequence coding for the promoter region of an ε-cyclase, and

b) at least one further ribonucleotide sequence which is substantially complementary to at least one part of the ribonucleotide sequence under a),

where a) and b) are connected together covalently, and further functional elements may be located where appropriate between a) and b).

18. The ribonucleic acid molecule as claimed in claim 17, where the promoter region of the ε-cyclase includes a sequence selected from the sequences as shown in SEQ ID NO: 1, 7 or 8.

19. A transgenic expression cassette, comprising

a) at least one promoter functional in plants, and

b) at least one nucleic acid sequence coding for a double-stranded RNA molecule as claimed in either of claims 15 or 16 or coding for a ribonucleic acid molecule as claimed in either of claims 17 or 18,

where at least one of said promoters and at least one of said nucleic acid sequences are functionally linked together, and the promoter is heterologous in relation to the nucleic acid sequence.

20. The transgenic expression cassette as claimed in claim 19, where the promoter is a promoter having specificity for the flower of plants.

21. A transgenic expression vector comprising a nucleic acid sequence as claimed in any of claims 12 to 14 or a transgenic expression cassette as claimed in any of claims 9, 10, 11, 19 or 20.

22. A transgenic organism comprising a nucleic acid sequence as claimed in any of claims 12 to 14, a double-stranded RNA as claimed in claim 15 or 16, a ribonucleotide sequence as claimed in claim 17 or 18, a transgenic expression cassette as claimed in any of claims 9, 10, 11, 19 or 20 or a transgenic expression vector as claimed in claim 21.

23. The transgenic organism as claimed in claim 22 selected from the group consisting of bacteria, yeasts, fungi, animal and plant organisms.

24. The transgenic organism as claimed in claim 22 selected from the group consisting of bacteria, yeasts, fungi, non-human animal and plant organisms or cells, cell cultures, parts, tissues, organs or propagation material derived therefrom.

25. The transgenic organism as claimed in claim 23 or 24 selected from the group of agricultural crop plants.

26. The use of an isolated nucleic acid sequence as claimed in any of claims 12 to 14, of a double-stranded RNA as claimed in claim 15 or 16, of a ribonucleotide sequence as claimed in claim 17 or 18, of a transgenic expression cassette as claimed in any of claims 9, 10, 11, 19 or 20, of a transgenic expression vector as claimed in claim 21 of a transgenic organism as claimed in any of claims 23 to 25 or cell cultures, parts, organs, tissues or transgenic propagation material derived therefrom in methods for the transgenic expression of nucleic acids or proteins.

27. The use of an isolated nucleic acid sequence as claimed in any of claims 12 to 14, of a double-stranded RNA as claimed in claim 15 or 16, of a ribonucleotide sequence as claimed in claim 17 or 18, of a transgenic expression cassette as claimed in any of claims 9, 10, 11, 19 or 20, of a transgenic expression vector as claimed in claim 21, or of a transgenic organism as claimed in any of claims 23 to 25 or cell cultures, parts, organs, tissues or transgenic propagation material derived therefrom for producing human or animal foods, seeds, pharmaceuticals or fine chemicals.

28. A method for producing human or animal foods, seeds, pharmaceuticals or fine chemicals, where a transgenic organism as claimed in any of claims 23 to 25 is cultured, and the desired human or animal foods, seeds, pharmaceuticals or fine chemical is produced and/or isolated using said organism.

29. A method for producing ketocarotenoids, where the mRNA amount and/or activity of at least one ε-cyclase is reduced by introducing at least one double-stranded RNA as claimed in claim 15 or 16, one ribonucleotide sequence as claimed in claim 17 or 18 or one transgenic expression cassette as claimed in either of claims 19 or 20.